

Serial No.: 09/938,714

REMARKS

Applicant conducted a Telephone Interview with the Examiner regarding the submission of Exhibits A and B in response to the Official Action filed on November 16, 2005. The Examiner was unable to read the Exhibits and suggested to divide the Exhibits into 8.5 x 11 pages. Attached is Exhibit B. Please note the Exhibit can be pieced together by referring to the attached grid. Exhibit A is being submitted in a separate transmission in order to prevent the pages of the Exhibits from being intermingled.

By submission of the 8.5 x 11 copies of Exhibit B, applicant respectfully submits that Amendment B is fully responsive to the Official Action dated March 1, 2005. Further, applicant respectfully requests reconsideration of Amendment B.

CONCLUSION

In light of the above amendments and remarks, it is respectfully submitted that the present application is now in proper condition for allowance, and such action is earnestly solicited.

If any small matter should remain outstanding after the Patent Examiner has had an opportunity to review the above Remarks, the Patent Examiner is respectfully requested to telephone the undersigned patent attorney in order to resolve these matters and avoid the Issuance of another Official Action.

Serial No.: 09/938,714

DEPOSIT ACCOUNT

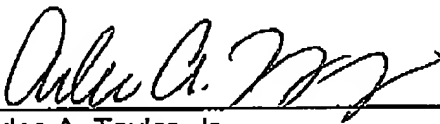
The Commissioner is hereby authorized to charge any fees associated with the filing of this correspondence to Deposit Account No. 50-0426.

Respectfully submitted,

JENKINS, WILSON &amp; TAYLOR, P.A.

Date: December 15, 2005

By:

  
Arles A. Taylor, Jr.  
Registration No. 39,395  
Customer No. 25297

AAT/BJO/alb

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PM JENKINS, WILSON & TAYLOR

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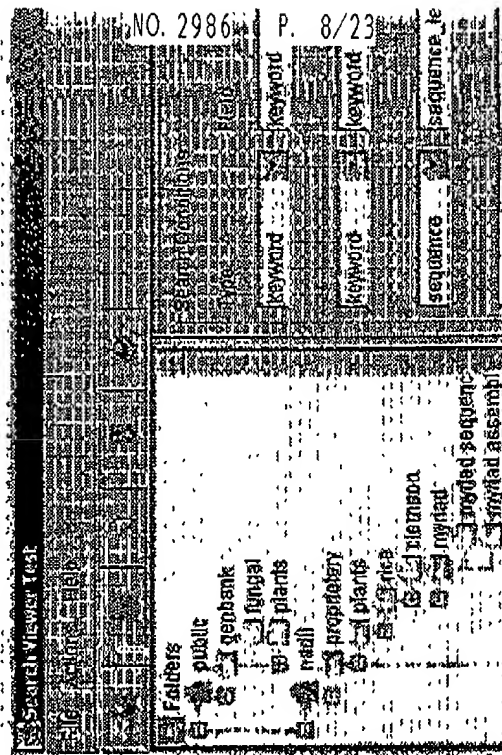
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## Frequently Asked Questions:

### 1. What is XML?

- The acronym stands for eXtensible Markup Language
- HTML is also XML, and both are derived from SGML (Standard Generalized Markup Language)
- It is a meta-language for representing structured data

### 2. What is the purpose of XML?

- Allows cross-platform formatting and organization of data
- Allows application and platform independent data exchange
- It separates content from its representation
- It facilitates the reuse of information

### 3. Where is XML used?

- E-commerce

A3

#### • Business-to-business communication

- Exchanging data of any kind without the need of file conversion
- Improved "smart" search engines on the web

#### 4. Is XML a standard?

- Yes, version 1.0 of the XML specification was accepted by the World Wide Web Consortium (W3C) as a recommendation on February 10, 1998.

#### 5. What do I need to create/view XML documents?

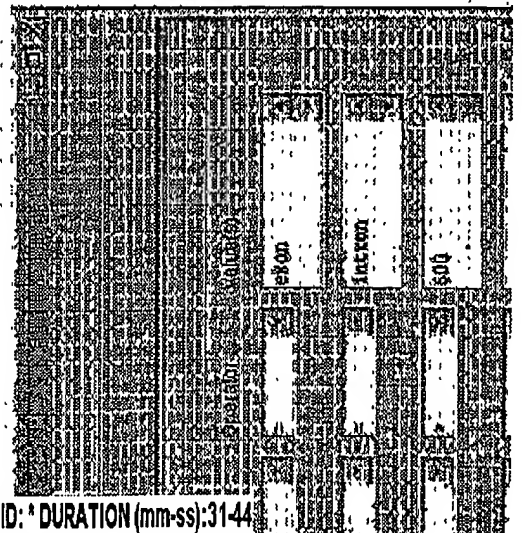
- XML is just text, so any text editor can be used to view/edit files
- XML documents can be viewed in a tree-like form in the Internet Explorer

#### 6. What is XSL?

- The acronym stands for eXtensible Style Language
- Similar to HTML's Cascading Style Sheets (CSS)
- Used to transform XML into HTML to be viewed in a browser



# STING TUG EXGAIN



NO. 2986. P. 12/23

SEARCHED INDEXED  
SERIALIZED FILED  
DEC 15 2005  
FBI - NEW YORK

XML

B1

File

Xml  
Loader

Configuration

| Configuration    | Item   | Value | Unit |
|------------------|--------|-------|------|
| some more plants | 362    |       |      |
| some plants      | 1426   |       |      |
| some plants      | 2051   |       |      |
| some more plants | 2032   |       |      |
| some more plants | 2052   |       |      |
| some more plants | 2027   |       |      |
| some more plants | 887    |       |      |
| some plants      | 6902   |       |      |
| some more plants | 1520   |       |      |
| some plants      | 5179   |       |      |
| some plants      | 150513 |       |      |

ifc XML output

B2

DEC. 15. 2005 3:00PM

JENKINS, WILSON&TAYLOR

NO. 2986 P. 14/23

```
<?xml version="1.0" encoding="ISO-8859-1" standalone="no" ?>
<table name="Sequence" schema="SAGE" >
  <table name="Sequence" schema="SAGE" >
    <field name="date_created" type="date" format="dd-mm-yyyy" />
    <field name="description" type="text" />
    <field name="sequence" type="text" />
    <field name="sequence_length" type="text" />
    <field name="sequence_name" type="text" />
    <field name="variable" type="text" />
    <field name="feature" type="text" />
    <field name="feature_height" type="text" />
    <field name="feature_description" type="text" />
    <field name="feature_end" type="text" />
    <field name="feature_start" type="text" />
    <field name="feature_type" type="text" />
    <field name="feature_sub_type" type="text" />
    <field name="feature_value" type="text" />
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    <field name="feature_value98" type="text" />
    <field name="feature_value99" type="text" />
    <field name="feature_value100" type="text" />
  </table>
</table>
```

**Fasta to XML** **Organisms** **Sage to XML**

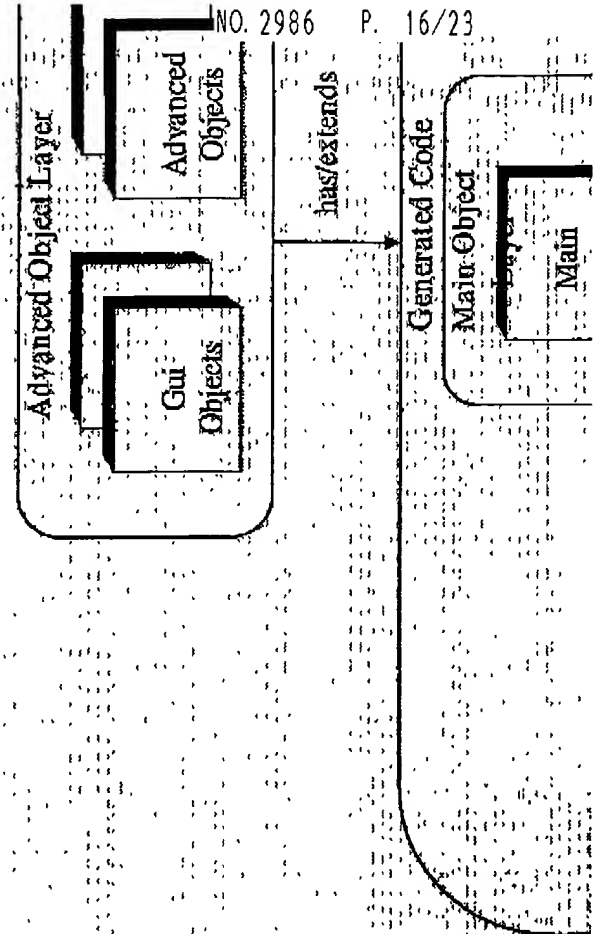
B3

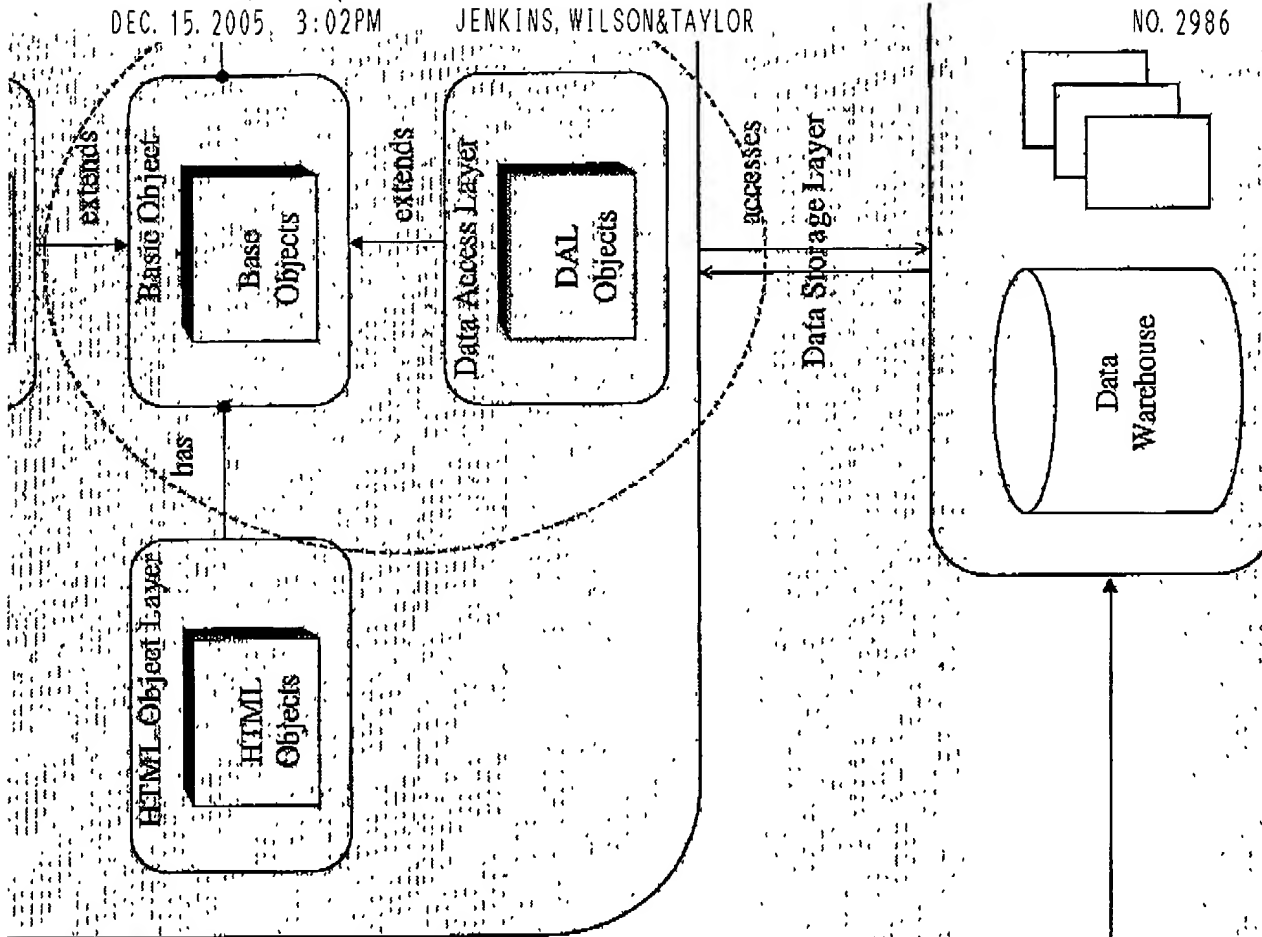
## Data

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第 2 版

COINTEGRATING  
BIOLOGICAL  
RECORDING  
ANALYSIS





Code Generation

Loading XML files

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**XML Quality to XML**  
**Maps to XML**  
**Access to XML**

3.



# Data

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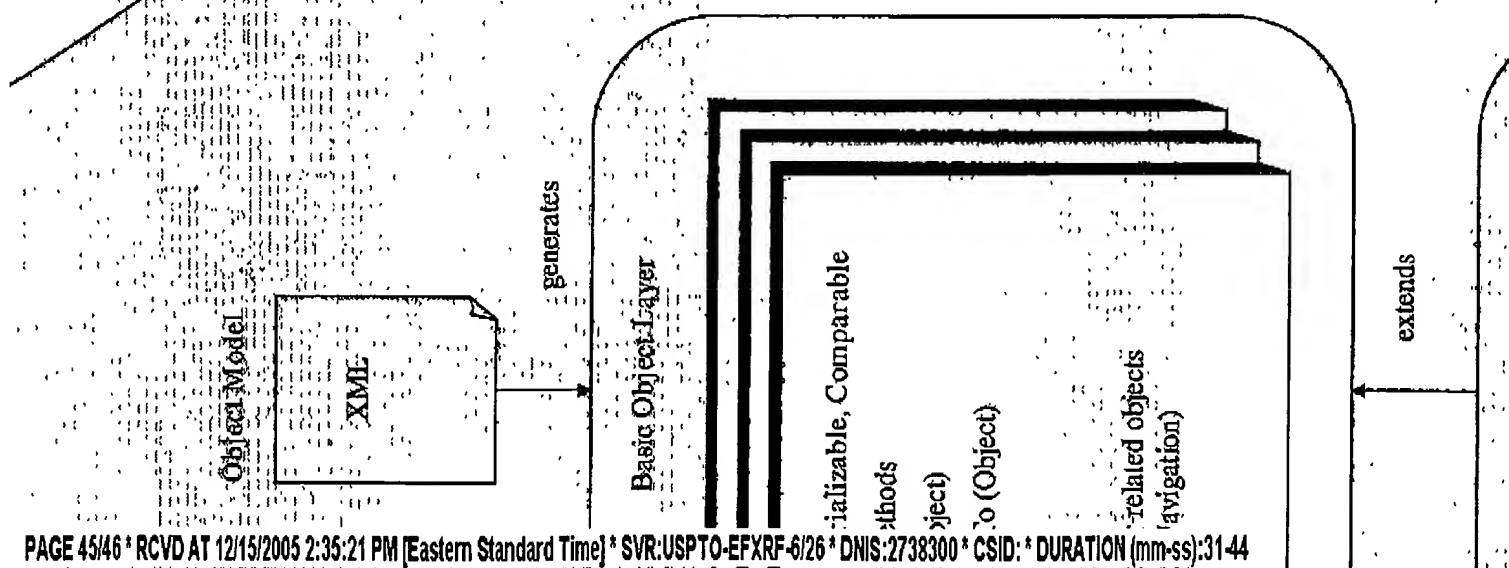
JENKINS

B2

generated code

XML Object Layer

XML  
Objects



# Actual Implementation

```

<Table name="Chromosome" duplicates="true">
  <PrimaryKey name="chromosome_id" type="long" />
  <ForeignKey name="organism_id" type="long" table="Organism"/>
  <ForeignKey name="source_id" type="long" table="Source"/>
  <Field name="chromosome_name" type="String" main="true"></Field>
  <Field name="chromosome_length" type="long"></Field>
</Table>
    
```

```

public class BaseChromosome extends BaseObject
implements java.io.Serializable, Comparable {

    public String getChromosome_name() {
        return chromosome_name;
    }

    public boolean equals(Object obj) {
        BaseChromosome chromosome= (BaseChromosome)obj;
        return (chromosome_length == chromosome.chromosome_length
            &&
            chromosome_name.equalsIgnoreCase(chromosome.chromosome_name)
        );
    }

    public Vector getChromosomeBands() {
        return chromosomebands;
    }
}
    
```

extends

D3

public class ChromosomeDAL extends BaseChromosome

Data-Access Object Layer

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Data Storage Layer

Data  
rehouse

```

public BaseObject findByPrimaryKey(QueryBroker broker) {
    String sql = "select * from Chromosome where chromosome_id=" + chromosome_id;
    BaseObject result = null;
    ResultSet r = broker.doQuery(sql);
    if (r==null) return null;
    try {
        if (r.next()) {
            result = getFromResultSet(r);
        }
        r.close();
    } catch (SQLException e) {
        e.printStackTrace();
    }
    return result;
}

public void loadChromosomeBands(QueryBroker broker) {
    String sql = "select ChromosomeBand.chromosome_band_id,
    ChromosomeBand.chromosome_id, ChromosomeBand.left_position,
    ChromosomeBand.right_position, ChromosomeBand.band_name,
    ChromosomeBand.band_color"
    +" from ChromosomeBand"
    +" where ChromosomeBand.chromosome_id=" + chromosome_id;
    ChromosomeBandDAL temp = new ChromosomeBandDAL();
    Vector res = temp.search(broker, sql);
    setChromosomeBands(res);
}

public ForeignKey[] getForeignKeys() {
    ForeignKey[] foreignkeys = {
        new ForeignKey("organism_id", "Organism"),
        new ForeignKey("source_id", "Source")
    };
    return foreignkeys;
}

```

D4

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